Docket 242/026 Express Mail EL199138787 US And the first man from the first the first that the

FIGURE 1

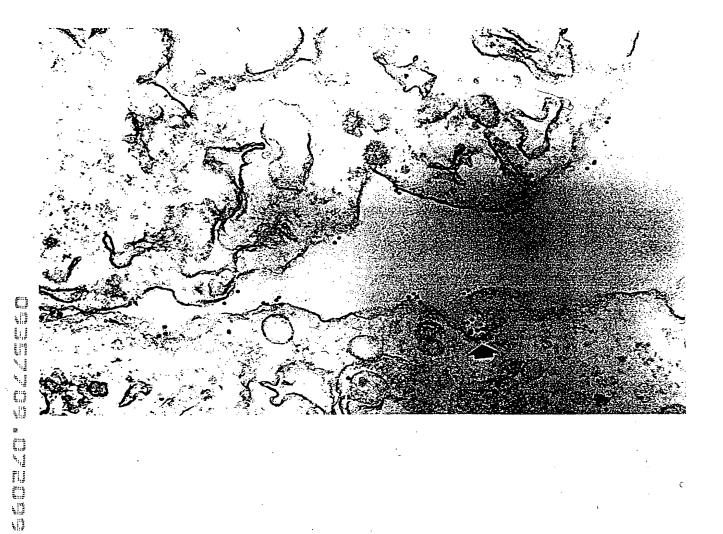
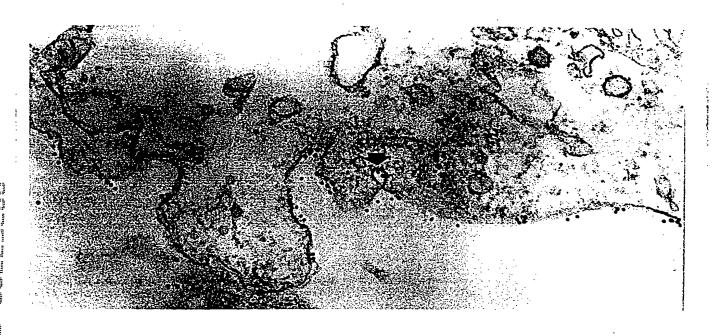
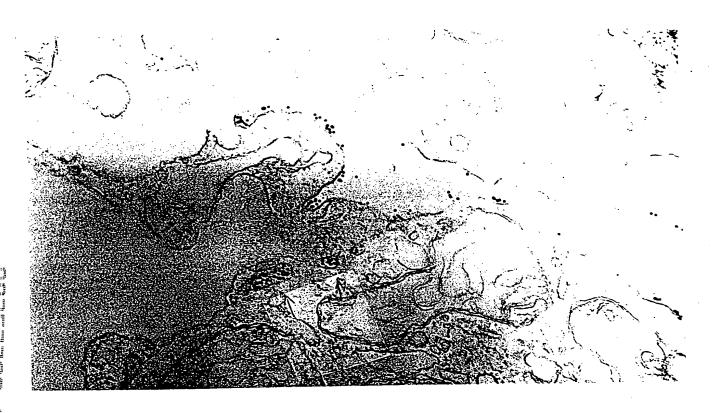
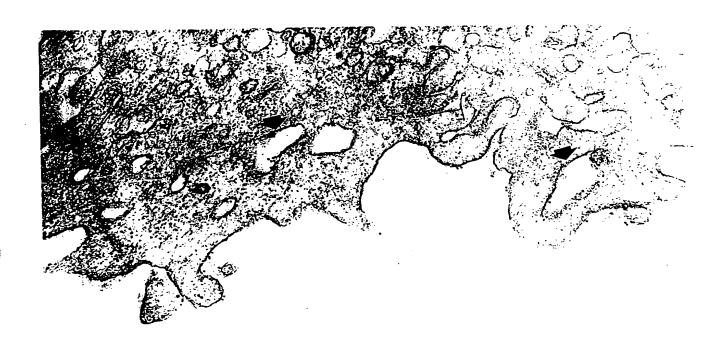
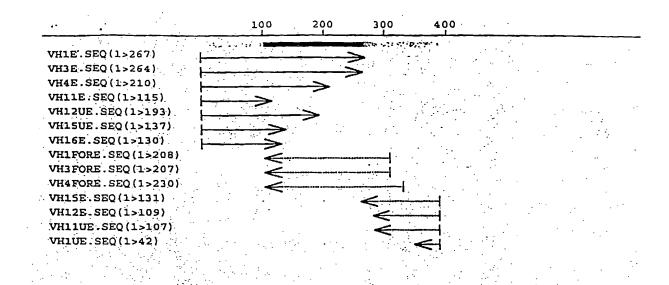


FIGURE 2









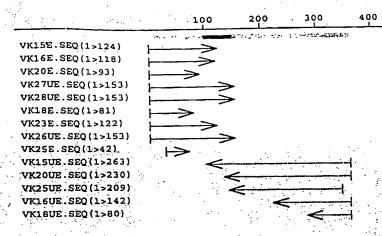
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			Enzymes: All 74 enzymes (No Filter) Settings: Linear, Certain Sites Only, Standard Genetic Code
			Dde I Ava II Alu I Ava II Eco57 I Pst I Sau96 I Pvu II Sau96 I Bsr I
SEQ. ID.	NO.	1	TCTCCTGTCAGGAACTGCAGGTGTCCTCTGAGGTCCAGCTGCAACAGTCTGGACCTGAACTGGTGAAG
SEQ. ID.	NO.	2	AGAGGACAGTCCTTGACGTCCACAGGAGAGACTCCAGGTCGACGTTGTCAGACCTTGACCACTTC
SEQ. ID. SEQ. ID.	NO.	3 4 5	SPVRNCRCPL GPAATVWT . TGE LLSGTAGVLSEVOLOOSGPELVK LSCOELOVSSLRSSCNSLOLNW . S
			Hph I Dra III   Bsp6 II   EcoR V   Bsr I
SEQ. ID.	NO.	1	CCTGGGACTTCAGTGAGGATATCCTGCAAGACTTCTGGATACACATTCACTGAATATACCATACACTGGG
SEQ. ID	NO.	2	GGACCCTGAAGTCACTCCTATAGGACGTTCTGAAGACCTATGTGTAAGTGACTTATATGGTATGTGACCC
SEQ. ID SEQ. ID SEQ. ID	NO.	3 4 5	AWDFSEDILOOFWIHIH.IYH!TLG PGTSVRISCKTSGYTFTEYTIHW LGLO.GYPARLLDTHSLNIPYTG
1			Hph I N∞ I Rsa I Kpn I
SEQ. ID	NO.	1	TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAAACATCAATCCTAACAATGGTGGTACCACCTA
\$∄Q. ID	NO.	2	ACTTCGTCTCGGTACCTTTCTCGGAACTCACCTAACCTTTGTAGTTAGGATTGTTACCACCATGGTGGAT
73.2	. NO. . NO.		EAEPWKEP. VOWKHOS. OWWY. HL VKOSHGKSLEWIGNINPNNGGTTY . SRAMERALSGLETSILTHV VPP
4.J - 4.D			Alu l
= -			Taq i Hae III Acc i Bsr i Rsa i Sac i
SEQ. ID	NO.	1	CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGGAGCTC
SEQ. ID		_	GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTTCAGGAGGTCATGTCGGATGTACCTCGAG
SEQ. ID		3 4 5	OSEVRGOGHIDCROVLOYSLHGA NOKFEDKATLTVDKSSSTAYMEL TIRSSRTRPH L TSPPVOPTWSS
		-	Sau961
ή,			Alu I Bsr I Dde I Hinf I Pst I Pvu II   Hae III
SEQ. ID			CGCAGCCTAACATCTGAGGATTCTGCAGTCTATTATTGTGCAGCTGGTTGGAACTTTGACTACTGGGGCC
SEQ. ID	. NO.	2	GCGTCGGATTGTAGACTCCTAAGACGTCAGATAATAACACGTLGACCAACCTTGAAACTGATGACCCCGG
SEQ. ID SEQ. ID SEQ. ID	. NO.	4	POPNI GFCSLLLCSWLEL LLGP RSLTSEDSAVYYCAAGWNFDYWG AA.HLRILOSIIVOLVGTLTTGA
			Alw26 I Ode I
SEQ. ID	. NO.	.1	AAGGCACCACTCTCACAGTCTCCTCAGCCAAAACGACACCC
SEQ. ID	. NO.	2	TTCCGTGGTGAGAGTGTCAGAGGAGTCGGTTTTGCTGTGGG
SEQ. ID	NO.	4	R H H S H S L L S Q N Q T Q G T T L T V S S A K T T P K A P L S Q S P Q P K R H P
SEQ. ID	. NO.	)	

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Lipman-Pearson Pro Ktuple: 2; Gap Pena Seq1(1>115) J591VH.PRO	otein Alignment alty: 4, Gap Length I Seq2(1>125) MUVHIIA.PRO	Penalty: 12 Similarity Index	Gap Number	Gap Length	Consensus Length	
(1>115)	(1>125)	75.6	2	10	125	
EVOLOOSGPELVKPO EVOLOOSGPELVKPO 410 460 F70 YNOKE KATITYDI	STSVRISCKTSGYTFT S:SV:ISCK:SGYTFT SASVKISCKASGYTFT 420 480 (SSSTAYMELRSLTSE (SSSTAYM:L.SLTSE KSSSTAYMOLSSLTSE	EYTI-HWVKO :Y : :WVKO DYYMNNWVKO :30  #90 DSAVYYCAAG DSAVYYCAG DSAVYYCARG	SHGKSLEWIGN SIGKSLEWIGN SPGKSLEWIGN 40 F	. INP.NGGI DINPGNGGT 50 100 NFDYWGQGT . FDYWGQG AFDYWGQG	:: FS - 	
LTVSS :TVSS VTVSS					*** *** ** 1	

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				Enzymes: All 74 enzymes (No Filter) Settings: Linear, Certain Sites Only, Standard Genetic Code Hoh I
	,		-	Alu l
SEQ.			_	TTATATGGAGCTGATGGGAACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGA 70 AATATACCTCGACTACCCTTGTAACATTACTGGGTTAGAGGGTTTAGGTACAGGTACAGTCATCCTCTCT
SEQ.				
SEQ.	ID.	NO.	12	LYGADGNIVMTOSPKSMSMSVGE YMELMGTL PNLPNPCPCO ER IIWS WEHCNDPISOIHVHVSRRE
SEQ.	ID.	NO.	13	
				Hae III   Bsr I
SEQ.	ID.	NO.	9	GGGTCACCTTGACCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTTCCTGGTATCAACAGAAACCAGA
SEQ.				CCCAGTGGAACTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTTGGTCT
SEQ.	ID.	NO.	11 12	R V T L T C K A S E N V V T Y V S W Y O O K P E G S P P A R P V R H W L L H F P G I N R N O G H L D L O G O . E C G Y L C F L V S T E T R
SEQ.	ID.	NO.	13	
				Mbo 1  Ava II Dpn 1  Hpa II Bsr 1 Bsa0 1  Rsa 1 Sau96 I Pvu I
				AW261 FOK1   1   1   1   1   1   1   1   1   1
SEQ.				
SEQ.				
SEQ.	ID.	NO.	12	S S L L N C
(SEQ	ID.	NO.	. 13	
≘ .				Mbo 1   Bsp6 II   Mbo II   Eco57 I
SEQ	. ID.	NO.	. 9	10TOCATCTCCAACAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTTCACTCTGACCAGTGTGCAGGCTGAAGACCTTGCAGATTCACTCTGACCAGTGTGCAGATTCACAGTGTGCAGGCTGAAGACCTTGCAGATTCACAGTGTGCAGGCTGAAGACCTTGCAGATTCACAGTGTGCAGGCTGAAGACCTTGCAGATTCACAGTGTAGATTCACAGTAGATTCACAGTGTAGATTCACAGTGTAGATTCACAGTGTAGATTCACAGTGTAGATTCACAGTGTAGATTCACAGTGTAGATTCACAGTGTAGATTCACAGTAGATTCACAGTGTAGATTCACAGTAGATTCACAGTAGATTCACAGTAGATTCACAGTAGATTCACAGAT
SEQ	ID.	. NO	. 10	TCACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTCACACGTCCGACTTCTGGAACGTCTAATAGTGA
SEQ SEQ	. ID.	. NO	. 11	S G S A T O F T L T I S S V C R L K T L O I I T
SEQ	. ID	. NO	. 13	3 W T C N N
				Avall Aud Rsal Sau961 Alul
٠			•	GTGGACAGGGTTACAGCTACCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGC
SEQ	. ID	. NO	. 9 . 10	
•				C C T K L F L K R A <sup>5</sup> A
SEQ	. ID . ID	. NO	. 12	2 V D R V T A R N "V R R G D Q A G N K T G . C
				randra de la companya de la company
	. ID			TGCACCAACTGTA  ACCITICATION 363.
	. ID	*		
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SEC	. ID	. NO	$\overline{1}$	2

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Docket 242/026 Express Mail EL199138787US

Lipman-Pearson Pro Ktuple: 2; Gap Pena Seq1(1>107) J591VK.PRO		Penalty: 12 Similarity Index	Gap Number	Gap Length	Consensus Length	
(1>107)	(1>109)	60.4	2	2	109	
F10 NIVMTOSPKSMSMSV :I MTOSP S:S S: DIOMTOSPSSLSASL 410  F60 F70 DRFTGSGSATDFTLT RF:GSGS:TD::LT SRFSGSGSGTDYSLT	G:RVT:TC:AS:: GDRVTITCRASODD 420 480 LSSVOAEDLADYHC	VYTYVSWYOOK : Y::WYOOK ISNYLNWYOOK 430 490 GOGYSY-PYTF OG:: P TF	P. SPKLLIY PGGSPKLLIY 40 ∳100 GGGTKLEIK GGGTKLEIK		b b	

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